

What is claimed is:

1. A nucleic acid molecule, comprising a nucleotide sequence that comprises:
 - a. a transcription regulatory region;
 - b. a transcription termination moiety;
 - c. a linking moiety; and
 - d. an open reading frame.
2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises dsDNA, or ssDNA.
3. The nucleic acid molecule of claim 2, wherein said nucleic acid molecule comprises dsDNA.
4. The nucleic acid molecule of claim 1, further comprising a ribosome binding sequence.
5. The nucleic acid molecule of claim 4, wherein said ribosome binding sequence comprises a Shine-Dalgarno sequence, a Kozak sequence, or an IRES.
6. The nucleic acid molecule of claim 5, wherein said ribosome binding sequence comprises a Shine-Dalgarno sequence.
7. The nucleic acid molecule of claim 1, wherein said transcription regulatory region is a prokaryotic or eukaryotic promoter.
8. The nucleic acid molecule of claim 7, wherein said transcription regulatory region is a prokaryotic promoter.
9. The nucleic acid molecule of claim 1, wherein said transcription termination moiety is a DNA binding protein or a sequence having secondary structure.
10. The nucleic acid molecule of claim 9, wherein said transcription termination moiety is a DNA binding protein.

11. The nucleic acid molecule of claim 1, wherein said linking moiety is a tRNA mimetic, biotin, digoxigenin, nitrilotriacetic acid, a nucleic acid sequence, a peptide nucleic acid sequence, or a peptide sequence.
12. The nucleic acid molecule of claim 11, wherein said linking moiety is a tRNA mimetic.
13. The nucleic acid molecule of claim 12, wherein said tRNA mimetic is puromycin.
14. The nucleic acid molecule of claim 1, wherein said open reading frame comprises a random sequence or sequence of interest.
15. The nucleic acid molecule of claim 1, further comprising a translational start codon.
16. The nucleic acid molecule of claim 8, wherein said at least one translational start codon is dAdTdG.
17. The nucleic acid of claim 1, further comprising a spacer region.
18. The nucleic acid molecule of one of claims 2, 4, 8, 9, 11, 14, 15, or 17, wherein said nucleic acid molecule is operably linked to a polypeptide encoded by said random sequence or sequence of interest.
19. The nucleic acid molecule of one of claim 18 wherein said nucleic acid molecule is covalently linked to a polypeptide encoded by said open reading frame.
20. A vector comprising the nucleic acid molecule of one of claims 1, 2, 4, 8, 9, 11, 14, 15, or 17.
21. The vector of claim 20, wherein said vector is a plasmid, a viral vector, a liposome, a microsphere, or a linear dsDNA molecule.
22. The nucleic acid of claim 18 bound to a substance of interest.

23. The nucleic acid molecule of claim 22, wherein said substance of interest is on a solid support.
24. The nucleic acid molecule of claim 22, wherein said substance of interest is on or within a cell.
25. The nucleic acid molecule of claim 22, wherein said cell is *ex vivo*.
26. The nucleic acid molecule of claim 22, wherein said cell is *in vivo* in a subject.
27. The nucleic acid molecule of claim 22, wherein said cell is a normal cell or an abnormal cell.
28. The nucleic acid molecule of claim 25, wherein said cell is an abnormal cell.
29. The nucleic acid molecule of claim 28, wherein said abnormal cell is a neoplastic cell or a virus infected cell.
30. The nucleic acid molecule of claim 22, wherein said substance of interest is on or within an etiological agent.
31. The nucleic acid molecule of claim 30, wherein said etiological agent is selected from the group consisting of a bacteria, a spore, a virus, a parasite or a prion.
32. The nucleic acid molecule of claim 22, wherein said nucleic acid molecule is bound to a solid support.
33. The nucleic acid molecule of claim 32, wherein said solid support is a chip or array, a bead, a matrix, a solid surface or a membrane.
34. The nucleic acid molecule of claim 22, wherein said substance of interest comprises at least one organic molecule, inorganic molecule, polymer, peptide, polypeptide, nucleic acid molecule, ribozyme, lipid, carbohydrate, small molecule, biomacromolecule or drug.

35. A library of nucleic acid molecules of one of claims 1, 2, 4, 8, 9, or 11.
36. The library of nucleic acid molecules of claim 35, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
37. A library of nucleic acid molecules of claim 22.
38. The library of nucleic acid molecules of claim 37, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
39. The library of nucleic acid molecules of any one of claims 35 to 38, wherein said library is contacted with at least one substance of interest.
40. The library of nucleic acid molecules of claim 39, wherein said at least one substance of interest is directly or indirectly bound on a solid support or in solution.
41. The library of nucleic acid molecules of claim 39, wherein said substance of interest is on or within a cell.
42. The nucleic acid molecule of claim 41, wherein said cell is *ex vivo*.
43. The nucleic acid molecule of claim 41, wherein said cell is *in vivo* in a subject.
44. The nucleic acid molecule of claim 41, wherein said cell is a normal cell or an abnormal cell.
45. The nucleic acid molecule of claim 44, wherein said cell is an abnormal cell.

46. The nucleic acid molecule of claim 45, wherein said abnormal cell is a neoplastic cell or a virus infected cell.
47. The nucleic acid molecule of claim 39, wherein said substance of interest is on or within an etiological agent.
48. The nucleic acid molecule of claim 47, wherein said etiological agent is selected from the group consisting of a bacteria, a virus, a parasite or a prion.
49. The library of claim 41, wherein said library of nucleic acid molecules is on a solid support.
50. A method for identifying a nucleic acid molecule, comprising:
 1. providing a nucleic acid molecule of claim 3, 4, 7, 9, 11, or 15;
 2. transcribing said nucleic acid molecule to provide a transcription complex, wherein said complex comprises a nucleic acid operably linked to a transcribed RNA;
 3. translating said transcribed RNA to form a nucleic acid-polypeptide complex, wherein said nucleic acid-polypeptide complex comprises a nucleic acid operably linked to a polypeptide that the nucleic acid encodes;
 4. contacting said nucleic acid-polypeptide complex with at least one substance of interest;
 5. selecting at least one complex that binds with said at least one substance of interest; and
 6. identifying said nucleic acid molecule.
51. The method of claim 50, wherein said contacting comprises conditions that promote binding of said complex to said substance of interest.
52. The method of claim 50, wherein said identifying comprises amplifying said random sequence or said nucleic acid sequence of interest.
53. The method of claim 50, wherein said substance of interest is on a solid support or in solution.

54. The method of claim 50, wherein said substance of interest is on or within a cell.
55. The method of claim 50, wherein said substance of interest is on or within an etiological agent.
56. The method of claim 50, wherein said at least one complex is on a solid support.
57. A nucleic acid molecule or nucleic acid sequence identified by the method of claim 50.
58. The method of claim 50, further comprising the step of sequencing the identified random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.
59. The method of claim 50, further comprising performing steps 1, 2, 3, 4, and 5 reiteratively.
60. The method of claim 50, further comprising performing steps 1, 2, 3, 4, 5, and 6 reiteratively.
61. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest, comprising:
 - 1) providing a nucleic acid molecule of claim 3, 4, 7, 9, 11, or 15;
 - 2) transcribing said nucleic acid molecule to provide a transcription complex, wherein said complex comprises a nucleic acid operably linked to a transcribed RNA;
 - 3) translating said transcribed RNA to form a nucleic acid-polypeptide complex, wherein said nucleic acid-polypeptide complex comprises a nucleic acid operably linked to a polypeptide that the nucleic acid encodes;
 - 4) contacting said nucleic acid-polypeptide complex with at least one substance of interest;

- 5) selecting at least one complex that binds with said at least one substance of interest; and
- 6) identifying said nucleic acid molecule.

62. The method of claim 61, wherein said contacting comprises conditions that promote binding of said transcript to said substance of interest.
63. The method of claim 61, wherein said identifying comprises amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.
64. The method of claim 61, wherein said substance of interest is on a solid support or in solution.
65. The method of claim 61, wherein said substance of interest is on or within a cell.
66. The method of claim 61, wherein said substance of interest is on or within an etiological agent.
67. A polypeptide identified by the method of claim 61.
68. The method of claim 61, further comprising the step of sequencing said identified polypeptide.
69. The method of claim 61, further comprising performing steps 1, 2, 3, 4, and 5 iteratively.
70. The method of claim 61, further comprising performing steps 1, 2, 3, 4, 5, and 6 iteratively.
71. A polypeptide identified by the method of claim 61.
72. The method of claim 61, further comprising the step of sequencing the identified polypeptide.

73. A method for identifying a test compound, comprising:
- a) contacting a target with a complex that comprises:
 - 1) a linking moiety;
 - 2) a nucleic acid molecule comprising an open reading frame; and
 - 3) a polypeptide encoded by said open reading frame; wherein said linking moiety is operably linked to said polypeptide;
 - b) identifying polypeptides bound with said target;
 - c) determining the structure of said polypeptide; and
 - d) identifying moieties that have structures that have space filling shapes that are similar to at least a portion of said polypeptide.
74. A test compound identified by method of claim 73.
75. A pharmaceutical composition identified by a method of claim 73.
76. A method for identifying a target, comprising:
- a) contacting a substance of interest with a complex that comprises:
 - 1) a linking moiety;
 - 2) a nucleic acid molecule comprising an open reading frame; and
 - 3) a polypeptide encoded by said open reading frame; wherein said linking moiety is operably linked to said polypeptide; and
 - b) identifying targets that bind with said complex.
77. A target identified by the method of claim 76.
78. A pharmaceutical target identified by the method of claim 76.

79. A nucleic acid molecule, comprising a nucleotide sequence that comprises:
- a linking moiety; and
 - a random sequence or sequence of interest.
80. The nucleic acid molecule of claim 79, wherein said nucleic acid molecule comprises dsDNA, ssDNA, or ssRNA.
81. The nucleic acid molecule of claim 80, wherein said nucleic acid molecule comprises ssDNA.
82. The nucleic acid molecule of claim 79, further comprising a ribosome stalling sequence.
83. The nucleic acid molecule of claim 82, wherein said said ribosome stalling sequence comprises poly(dA)_n or a region of strong secondary structure.
84. The nucleic acid molecule of claim 83, wherein said ribosome stalling sequence comprises poly(dA)_n.
85. The nucleic acid molecule of claim 84, wherein said poly(dA)_n is between five and 50 bases in length.
86. The nucleic acid molecule of claim 79, further comprising at least one translational start codon.
87. The nucleic acid molecule of claim 86, wherein said at least one translational start codon is dAdTdG.
88. The nucleic acid of claim 79, further comprising a translational control sequence.
89. The nucleic acid of claim 88, wherein said translational control sequence is a Shine-Dalgarno sequence.

90. The nucleic acid of claim 79, further comprising a spacer region.
91. The nucleic acid of claim 79, wherein said linking moiety is a tRNA mimetic.
92. The nucleic acid of claim 91, wherein said linking moiety is puromycin.
93. The nucleic acid molecule of one of claims 80, 82, 86, 88, or 92, wherein said nucleic acid molecule is operably linked to a polypeptide encoded by said random sequence or sequence of interest.
94. The nucleic acid molecule of one of claim 93 wherein said nucleic acid molecule is covalently linked to a polypeptide encoded by said open reading frame.
95. A vector comprising the nucleic acid molecule of one of claims 80, 82, 86, 88, or 92.
96. The vector of claim 95, wherein said vector is a plasmid, a viral vector, a liposome, a microsphere, or a linear dsDNA molecule.
97. The nucleic acid of claim 93 bound to a substance of interest.
98. The nucleic acid molecule of claim 97, wherein said substance of interest is on a solid support.
99. The nucleic acid molecule of claim 98, wherein said substance of interest is on or within a cell.
100. The nucleic acid molecule of claim 99, wherein said cell is *ex vivo*.
101. The nucleic acid molecule of claim 99, wherein said cell is *in vivo* in a subject.
102. The nucleic acid molecule of claim 99, wherein said cell is a normal cell or an abnormal cell.

103. The nucleic acid molecule of claim 102, wherein said cell is an abnormal cell.
104. The nucleic acid molecule of claim 103, wherein said abnormal cell is a neoplastic cell or a virus infected cell.
105. The nucleic acid molecule of claim 97, wherein said substance of interest is on or within an etiological agent.
106. The nucleic acid molecule of claim 105, wherein said etiological agent is selected from the group consisting of a bacteria, a spore, a virus, a parasite or a prion.
107. The nucleic acid molecule of claim 97, wherein said nucleic acid molecule is bound to a solid support.
108. The nucleic acid molecule of claim 107, wherein said solid support is a chip or array, a bead, a matrix, a solid surface or a membrane.
109. The nucleic acid molecule of claim 97, wherein said substance of interest comprises at least one organic molecule, inorganic molecule, polymer, peptide, polypeptide, nucleic acid molecule, ribozyme, lipid, carbohydrate, small molecule, biomacromolecule or drug.
110. A library of nucleic acid molecules of one of claims 80, 82, 86, or 88.
111. The library of nucleic acid molecules of claim 110, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
112. A library of nucleic acid molecules of claim 97.
113. The library of nucleic acid molecules of claim 112, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.

114. The library of nucleic acid molecules of any one of claims 110 to 113, wherein said library is contacted with at least one substance of interest.
115. The library of nucleic acid molecules of claim 114, wherein said at least one substance of interest is directly or indirectly bound on a solid support or in solution.
116. The library of nucleic acid molecules of claim 114, wherein said substance of interest is on or within a cell.
117. The nucleic acid molecule of claim 116, wherein said cell is *ex vivo*.
118. The nucleic acid molecule of claim 116, wherein said cell is *in vivo* in a subject.
119. The nucleic acid molecule of claim 116, wherein said cell is a normal cell or an abnormal cell.
120. The nucleic acid molecule of claim 119, wherein said cell is an abnormal cell.
121. The nucleic acid molecule of claim 120, wherein said abnormal cell is a neoplastic cell or a virus infected cell.
122. The nucleic acid molecule of claim 114, wherein said substance of interest is on or within an etiological agent.
123. The nucleic acid molecule of claim 122, wherein said etiological agent is selected from the group consisting of a bacteria, a virus, a parasite or a prion.
124. The library of claim 116, wherein said library of nucleic acid molecules is on a solid support.

125. A method for identifying a nucleic acid molecule or sequence, comprising:
- 1) providing at least one nucleic acid molecule of claim 80, 82, 86, or 88;
 - 2) translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest;
 - 3) contacting said at least one complex with at least one substance of interest;
 - 4) selecting at least one complex that binds with said at least one substance of interest; and
 - 5) identifying said random sequence or said nucleic acid sequence of interest.
126. The method of claim 125, wherein said contacting comprises conditions that promote binding of said complex to said substance of interest.
127. The method of claim 125, wherein said identifying comprises amplifying said random sequence or said nucleic acid sequence of interest.
128. The method of claim 125, wherein said substance of interest is on a solid support or in solution.
129. The method of claim 125, wherein said substance of interest is on or within a cell.
130. The method of claim 125, wherein said substance of interest is on or within an etiological agent.
131. The method of claim 125, wherein said at least one complex is on a solid support.
132. A nucleic acid molecule comprising a random sequence or nucleic acid sequence or nucleic acid molecule identified by the method of claim 125.
133. The method of claim 125, further comprising the step of sequencing the identified

random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.

134. The method of claim 125, further comprising performing steps 1, 2, 3 and 4 reiteratively.
135. The method of claim 125, further comprising performing steps 1, 2, 3, 4, and 5 reiteratively.
136. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest, comprising:
 1. providing at least one nucleic acid molecule of claims 80, 82, 86, or 88;
 2. translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
 3. contacting said at least one complex with at least one substance of interest;
 4. selecting at least one complex that binds with said at least one substance of interest; and
 5. identifying said polypeptide in said complex.
137. The method of claim 136, wherein said contacting comprises conditions that promote binding of said transcript to said substance of interest.
138. The method of claim 136, wherein said identifying comprises amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.
139. The method of claim 136, wherein said substance of interest is on a solid support or in solution.
140. The method of claim 136, wherein said substance of interest is on or within a cell.

141. The method of claim 136, wherein said substance of interest is on or within an etiological agent.
142. A polypeptide identified by the method of claim 136.
143. The method of claim 136, further comprising the step of sequencing said identified polypeptide.
144. The method of claim 136, further comprising performing steps 1, 2, 3 and 4 reiteratively.
145. The method of claim 136, further comprising performing steps 1, 2, 3, 4 and 5 reiteratively.
146. A polypeptide identified by the method of claim 136.
147. The method of claim 136, further comprising the step of sequencing the identified polypeptide.
148. A method for identifying a test compound, comprising:
- a) contacting a target with a complex that comprises:
 - 1) a linking moiety;
 - 2) a random sequence or a sequence of interest that encodes a polypeptide; and
 - 3) a polypeptide encoded by said random sequence or sequence of interest;wherein said linking moiety is operably linked to said polypeptide;
 - b) identifying polypeptides bound with said target;
 - c) determining the structure of said polypeptide; and
 - d) identifying moieties that have structures that have space filling shapes that are similar to at least a portion of said polypeptide.
149. A test compound identified by method of claim 148.

150. A pharmaceutical composition identified by a method of claim 148.
151. A method for identifying a target, comprising:
- a) contacting a substance of interest with a complex that comprises:
 - 1) a linking moiety; and
 - 2) a random sequence or sequence of interest; and
 - 3) a polypeptide encoded by said random sequence or sequence of interest;wherein said linking moiety is operably linked to said polypeptide; and
 - b) identifying targets that bind with said complex.
152. A target identified by the method of claim 151.
153. A pharmaceutical target identified by the method of claim 151.